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Research Article

Taxonomic novelties of *Dothiorella* and additions to Botryosphaeriaceae from Yunnan, China

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Abstract

Botryosphaeriaceae is the largest family in Botryosphaeriales, consisting of 22 genera. Members of this family have cosmopolitan distribution, occurring in various life modes: endophytic, saprobic and pathogenic, mainly associated with plants. This study aims to investigate plant-associated saprobic microfungi in Yunnan, China. Here, we establish two novel species in *Dothiorella*, namely *D. fusiformis* and *D. swieteniae*. Both sexual and asexual morphs are provided for *D. fusiformis*. Additionally, we report two new host records of *Barriopsis archontophoenicis* S. Konta, Boonmee & K.D. Hyde and *D. camelliae* W.Li Li & Jian K. Liu. Taxonomic boundaries were confirmed based on morphological characteristics coupled with phylogenetic analyses using maximum likelihood (ML) and Bayesian inference (BI) analyses of combined SSU, LSU, ITS, *β-tubulin* and *tef*1-α sequences. Furthermore, the detailed illustrations, comprehensive descriptions, and taxonomic justifications are provided for each species. This study expands our understanding of the taxonomy, diversity and ecological relationships of Botryosphaeriaceae species in China by introducing new species and reporting new host and geographic records.

Key words: 2-new species, 2-new host records, Dothideomycetes, morphology, phylogeny

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Introduction

Botryosphaeriaceae was established by Theissen and Sydow (1918), with *Botryosphaeria* Ces. & De Not as the type genus. Over the years, Botryosphaeriaceae and its genera have undergone several taxonomic revisions. Phillips et al. (2008) examined the species with brown ascospores and introduced five more genera to Botryosphaeriaceae, providing accurate classification of *Diplodia* and *Lasiodiplodia*. Damm et al. (2007) showed that *Aplosporella* belongs to Botryosphaeriaceae, while Rojas et al. (2008) confirmed that *Endomelanco-*

niopsis is also part of the same family. Furthermore, Phillips and Alves (2009) considered *Melanops* as an additional genus in Botryosphaeriaceae. Liu et al. (2012) included 29 genera in this family based on morpho-molecular data. Comprehensive descriptions and keys for 17 genera in the family were provided by Phillips et al. (2013). Later, 24 well-defined genera were accepted in Botryosphaeriaceae based on morphology and molecular evidence (Burgess et al. 2019; Garcia et al. 2021). Currently, 22 genera are included in this family, forming clearly separate monophyletic clades. Botryosphaeriaceae represents the largest family within Botryosphaeriales (Zhang et al. 2021; Wijayawardene et al. 2022).

Species of Botryosphaeriaceae have a worldwide distribution, inhabiting a wide range of monocotyledonous and dicotyledonous hosts. They occur on different substrates viz. woody branches, leaves, stems, grass culms, twigs, and in the thalli of lichens (Barr 1987; Denman et al. 2000; Mohali et al. 2007; Lazziz-era et al. 2008; Marincowitz et al. 2008). These species have been reported as endophytes (Slippers and Wingfield 2007), pathogens, opportunistic pathogens (Chethana et al. 2016), or saprobes (Schoch et al. 2006), in agricultural crops, ornamental plants, and forest hosts, primarily in terrestrial ecosystems (Batista et al. 2021). Many Botryosphaeriaceae members, specifically species of *Botryosphaeria*, *Diplodia*, *Dothiorella*, *Lasiodiplodia*, and *Neofusicoccum*, have been recognized as pathogens that cause blights, cankers, dieback diseases as well as fruit-rot diseases in ecologically and economically important plants in forests and agricultural fields worldwide (Phillips et al. 2013; Slippers et al. 2013; Zhou et al. 2015; Phillips et al. 2019).

Saccardo (1880) introduced *Dothiorella* with *D. pyrenophora* Berk. ex Sacc. as the type species. Both sexual and asexual morphs have been described in this genus. The sexual morph is characterized by erumpent or superficial ascomata, bitunicate, fissitunicate asci and pigmented, and septate ascospores, while asexual morph exhibits immersed, erumpent conidiomata with hyaline, holoblastic conidiogenous cells (Phillips et al. 2013). Interestingly, the conidia become brown and 1-septate while still attached to the conidiogenous cells (Phillips et al. 2005; Dissanayake et al. 2016; Hongsanan et al. 2020). *Dothiorella* species occur on a wide range of hosts as endophytes, saprobes or pathogens (Phillips et al. 2013; Dissanayake et al. 2016; Jayawardena et al. 2019). The majority of *Dothiorella* species are plant pathogens or saprobes on a variety of woody hosts and they have a cosmopolitan distribution (Li et al. 2014). Currently, 348 species are listed in Index Fungorum (2026), while 336 epithets are listed under *Dothiorella* in Species Fungorum (2026). However, molecular data are available for only 60 species in GenBank (Zhang et al. 2025).

Barriopsis was introduced with *B. fusca* (N.E. Stevens) A.J.L. Phillips, A. Alves & Crous as the type species (Phillips et al. 2008). The sexual morph of this genus is characterized by bitunicate asci and brown ascospores that are widest in the middle, and lack terminal apiculi (Phillips et al. 2008). Lasiodiplodia-like asexual morph of this genus is characterized by initially hyaline, aseptate, thick-walled conidia, becoming dark brown and septate with irregular longitudinal striations at maturity (Phillips et al. 2008). However, compared to *Lasiodiplodia*, conidia of *Barriopsis* are striate at the early stage and striations visible on hyaline conidia while attached to conidiogenous cells (Abdollahzadeh et al. 2009). Currently, seven *Barriopsis* species are listed in Index Fungorum (2026).

Botryosphaeriaceae species occur worldwide and have different lifestyles, making further taxonomic and ecological analyses prerequisites. During our investigations of plant-associated microfungi in Yunnan, China, we collected and isolated five Botryosphaeriaceae taxa. In this study, we introduce two novel *Dothiorella* species with two new host records of *Barriopsis* and *Dothiorella*. Morphological illustrations, detailed descriptions, multigene phylogenetic analyses with maximum likelihood (ML) and Bayesian inference (BI) analyses confirm the phylogenetic placement of these newly isolated fungal taxa. Taxonomic notes with appropriate justifications for each taxon were also provided.

Materials and methods

Specimen collections, morphological studies and isolations

Fresh fungal samples were collected in different forest sites in Yunnan, China in July – September 2025. Specimens were enclosed in zip-loc plastic bags and brought to the laboratory. The samples were examined for morphology following the methodology described in Rathnayaka et al. (2024). Both macro- and micro- morphological characters were examined using a LEICA IVESTA 3 stereomicroscope (Leica Microsystems, Germany), and LEICA DM2500 compound microscope (Leica Microsystems, Germany), respectively and characters were photographed with a Canon 550D digital camera fitted to the compound microscope. Measurements were made with ZEN2 (blue edition) software and calculated with the Tarosoft (R) Image Frame Work program. Photographs were processed, and photo plates were prepared with Adobe Photoshop CS3 Extended version 10.0 software (Adobe Systems, USA).

Single spore isolations were carried out for fungal isolation as described in Senanayake et al. (2020) by using potato dextrose agar (PDA) media plates and incubated at 25 °C. Pure cultures were obtained by sub culturing, and culture characters were recorded after one week. The dried specimens were deposited at the fungarium of the Kunming Institute of Botany Academia Sinica (**HKAS**) and living cultures were deposited at the Germplasm Bank of Wild Species Culture Collection (**GBWSCC**). Index Fungorum numbers were obtained (http://www.indexfungorum.org) for the novel taxa.

DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from fresh mycelium (50–100 mg) using TIANGEN Plant Genomic DNA Kit (Tiangen Biotech, Beijing) by following the manufacturer's instructions. Polymerase chain reactions (PCR) were performed for a small subunit of nuclear ribosomal RNA (SSU), a large subunit of nuclear ribosomal RNA (LSU), internal transcribed spacers region (ITS), partial translation elongation factor 1-α gene (*tef*1-α) and beta-tubulin (*β-tubulin*) genes. The relevant PCR thermal cycles with the conditions are given in Table 1. PCR reactions were carried out in a final volume of 50 µl, which contained 21 µl of deionized water, 25 µl of 2× Power Taq PCR Master Mix (CWBIO, China), 1 µl of each forward and reverse primers and 2 µl of genomic DNA. PCR products were visualized on 1.5% agarose gels containing the Safeview DNA stain (Biosharp Life Sciences, China) and sequenced at Sangon Biotech sequencing laboratory

Table 1. Gene regions used in the study with PCR primers, conditions and references.

Gene region	Primers	PCR conditions	Reference(s)
SSU	NS1/NS4	95 °C, 3 min, (95 °C, 30 s, 55 °C, 50 s, 72 °C, 30 s) × 35 cycles, 72 °C, 10 min	White et al. (1990)
LSU	LR0R/LR5	95 °C: 3 min, (95 °C: 30 s, 55 °C:50 s, 72 °C: 30 s) × 35 cycles, 72 °C, 10 min	Vilgalys and Hester (1990)
ITS	ITS4/ITS5	95 °C: 3 min, (95 °C: 30 s, 55 °C:50 s, 72 °C: 30 s) × 35 cycles, 72 °C, 10 min	White et al. (1990)
*tef*1-α	EF1–728F/ EF1–986R	95 °C: 5 min, (94 °C: 30 s, 55 °C:45 s, 72 °C: 90 s) × 30 cycles, 72 °C, 10 min	Carbone and Kohn (1999)
β-tubulin	Bt2a/Bt2b	95 °C: 5 min, (94 °C: 30 s, 55 °C:45 s, 72 °C: 90 s) × 30 cycles, 72 °C, 10 min	Glass and Donaldson (1995)

(China). The remaining extracted DNA was stored at 4 °C for a short-term and –20 °C for long- term storage. Newly generated nucleotide sequences were deposited in GenBank (Table 2).

Phylogenetic analyses

The quality of the sequence chromatograms was checked manually using the BioEdit v 7.0.9.0 software (Hall 1999). Newly generated sequences were initially subjected to the BLASTn search engine at NCBI to observe more similar searches and related literature was referred to the recent taxonomic updates (Rathnayaka et al. 2022; Wang et al. 2025; Zhou et al. 2025). Sequences generated from this study and isolates retrieved from the GenBank are shown in Table 2. Each locus (SSU, LSU, ITS, *tef*1-α and *β-tubulin*) was aligned individually with MAFFT 6.864b (Katoh et al. 2019) and trimmed using trimAl v1.2 software in gappyout mode (Capella-Gutiérrez et al. 2009). Single gene and multi-gene aligned datasets were analysed separately using ML and BI. MrModeltest v. 2.2 (Nylander 2004) under the AIC (Akaike Information Criterion) implemented in PAUP v. 4.0b10 to find out the best fit models for BI and ML analyses. The GTR+G model was selected as the best model for both ML and BI analyses for each gene region.

The ML analyses were performed using IQ-Tree with bootstrap support obtained from 1,000 pseudoreplicates (Nguyen et al. 2015; Chernomor et al. 2016). The BI analyses were conducted with MrBayes v. 3.2.6 (Ronquist et al. 2012). The Markov Chain Monte Carlo (MCMC) algorithm of six chains was initiated for 1,000,000 generations. The trees were sampled at every 1000th generation, resulting in 1,000 trees. The first 10% of trees were discarded as the burn-in phase, while the remaining 90% were used to calculate the posterior probabilities (PP) in the majority rule consensus tree. Phylograms were visualized with the FigTree v1.4.0 program (Rambaut 2012) and reorganized in Microsoft PowerPoint (2010).

Results

Phylogenetic analyses

For *Dothiorella*, the combined LSU, ITS, *tef*1-α and *β-tubulin* dataset including 71 taxa was used with *Neofusicoccum luteum* (CBS 562.92 and CMW 41365) as the outgroup taxa. Related sequences were obtained from GenBank and related literature (Rathnayaka et al. 2022; Wang et al. 2025; Zhou et al. 2025). Final sequence alignment consisted of 2,015 characters including gaps (LSU =

Table 2. Taxa used in the phylogenetic analyses and their GenBank accession numbers. Newly introduced taxa and two extant species generated in this study are indicated in blue and type strains are indicated in bold.

Species	Strain no.	GenBank accession no.				
		SSU	LSU	ITS	*tef*1-α	*β-tubulin*
Alanphillipsia aloeicola	**CBS 138896**	N/A	MH878642	KP004444	N/A	–
Alanphillipsia aloeigena	**CPC 21286**	N/A	KF777193	KF777137	N/A	–
Barriopsis archontophoenicis	**MFLUCC 14-1164**	NG 063609	KX235307	KX235306	N/A	–
Barriopsis archontophoenicis	MFLU 20-0523	MT876121	MT876523	MT876524	MT897877	–
Barriopsis archontophoenicis	GBWSCCF120264	PX498709	PX498707	PX498655	PX562762	N/A
Barriopsis archontophoenicis	HKAS 151750	N/A	PX498708	PX498656	N/A	N/A
Barriopsis caryotae	**UESTCC:23.0407**	N/A	PQ166771	PQ181882	PQ166410	PQ390669
Barriopsis iraniana	**IRAN 1448C**	KF766231	KF766318	FJ919663	FJ919652	–
Barriopsis iraniana	IRAN1450C	–	–	FJ919667	FJ919656	–
Barriopsis menglaensis	**KUMCC 21-0578**	PQ206508	PQ206506	PQ206504	PQ218693	- –
Barriopsis stevensiana	**CBS 174.26**	KF766230	DQ377857	EU673330	EU673296	–
Barriopsis stevensiana	MFLUCC 11-0420	MN582689	MN582755	MN582740	–	–
Barriopsis tectonae	**MFLUCC 12-0381**	–	–	KJ556515	KJ556516	–
Barriopsis thailandica	MFLUCC 14-1190	–	–	KY115675	KY115676	–
Dothiorella acacicola	**CPC 26349**	–	KX228320	NR_145255	KX228376	N/A
Dothiorella acericola	KUMCC 18-0137	–	N/A	MK359449	MK361182	N/A
Dothiorella albiziae	**MFLUCC 22-0057**	–	ON751764	ON751762	ON799588	ON799590
Dothiorella alpina	CGMCC 3.18001	–	N/A	KX499645	KX499651	N/A
Dothiorella baihuashanensis	**CFCC 58549**	–	N/A	OQ651168	OQ692934	OQ692928
Dothiorella brevicollis	**CMW 36463**	–	NG_069098	NR_111703	JQ239390	JQ239371
Dothiorella camelliae	**CGMCC 3.24158**	–	N/A	OQ190531	OQ241464	OQ275064
Dothiorella camelliae	GBWSCCF110208	–	PX499329	PX499328	N/A	PX562763
Dothiorella capri-amiss	CBS:121763	–	KX464301	EU101323	EU101368	KX464850
Dothiorella casuarini	CBS 120688	–	MH874647	DQ846773	DQ875331	N/A
Dothiorella chiangmaiensis	MFLU 22-0161	–	N/A	NR_187083	OP614929	N/A
Dothiorella citricola	ICMP16828	–	EU673242	EU673323	EU673290	EU673145
Dothiorella citrimurcotticola	CGMCC 3.20394	–	N/A	MW880661	MW884164	MW884193
Dothiorella diospyricola	**CBS 145972**	–	N/A	MT587398	MT592110	MT592581
Dothiorella dulcispinae	CMW 36460	–	NG_069097	NR_111702	JQ239387	JQ239373
Dothiorella eriobotryae	**CBS 140852**	–	MH878199	KT240287	KT240262	MT592582
Dothiorella franceschinii	**CBS 147722**	–	N/A	NR_198362	OQ067247	N/A
Dothiorella heterophyllae	**CMW46458**	–	N/A	MN103794	MH548348	MH548324
Dothiorella fusiformis	**GBWSCCF120274**	–	PX727435	PX727439	N/A	PX730059
Dothiorella fusiformis	HKAS 151748	–	PX727436	PX727440	N/A	PX730060
Dothiorella fusiformis	**GBWSCCF120275**	–	PX727437	PX727441	N/A	PX730061
Dothiorella fusiformis	HKAS 151752	–	PX727438	PX727442	N/A	PX730062
Dothiorella hortiarborum	**CFCC 70756**	–	N/A	PP188524	PP723042	PP566662
Dothiorella iranica	**IRAN1587C**	–	NG_228749	KC898231	KC898214	KX464856
Dothiorella koae	CMW 48017	–	N/A	MH447652	MH548338	MH548327
Dothiorella lampangensis	MFLUCC 18-0232	–	N/A	NR_163336	MK340869	MK412874
Dothiorella longicollis	CBS 122068	–	NG_069903	EU144054	EU144069	KF766130
Dothiorella macadamiae	SDBR-CMU513	–	N/A	PQ699725	PQ758593	PQ736694
Dothiorella magnoliae	**CFCC 51563**	–	N/A	NR_191055	KY213686	N/A
Dothiorella mangifericola	**CBS 121760**	–	N/A	EU101290	EU101335	KX464877
Dothiorella mangifericola	IRAN1584C	–	N/A	KC898221	KC898204	N/A

Species	Strain no.	GenBank accession no.				
		SSU	LSU	ITS	*tef*1-α	*β-tubulin*
Dothiorella moneti	**MUCC505**	–	EF591937	EF591920	EF591971	EF591954
Dothiorella. oblonga	**CBS 121765**	–	KX464318	NR_137689	EU101345	N/A
Dothiorella obovata	**MFLUCC 22-0058**	–	ON751765	ON751763	ON799589	ON799591
Dothiorella ovata	**MFLUCC 23-0035**	–	OR020691	OR052059	OR030456	OR030474
Dothiorella plurivora	IRAN1557C	–	N/A	KC898225	KC898208	N/A
Dothiorella pretoriensis	**CMW 36480**	–	JQ239418	JQ239405	JQ239392	JQ239376
Dothiorella prunicola	CAP187	–	EU673232	EU673313	EU673280	EU673100
Dothiorella pugeense	SICAUCC 23-0142	–	PP862534	PP844870	PV220917	PV220918
Dothiorella rhamni	**MFLUCC 14-0902**	–	KU246382	KU246381	MF398945	N/A
Dothiorella rosacearum	**MFLUCC 23-0014**	–	OR052043	OR052061	OR030458	OR030476
Dothiorella rosulata	**CBS 121760**	–	NG_069178	NR_136991	EU101335	KX464877
Dothiorella samentorium	**CBS 128309**	–	MH876298	HQ288218	MT592106	MT592577
Dothiorella santali	**MUCC509**	–	EF591941	EF591924	EF591975	EF591958
Dothiorella saprophytica	MFLUCC 23-0210	–	N/A	OR527239	OR532455	OR532454
Dothiorella sarmentorum	MFLUCC 17-0242	–	KY815014	KY797637	N/A	MT592585
Dothiorella sarmentorum	CBS 115041	–	AY928053	AY573202	AY573222	EU673096
Dothiorella sarmentorum	MFLUCC 17-0951	–	N/A	MG828897	MG829267	MT592592
Dothiorella sarmentorum	**CBS 392.80**	–	N/A	KX464133	KX464626	KX464897
Dothiorella sarmentorum	IRAN1579C	–	N/A	KC898234	KC898217	N/A
Dothiorella sarmentorum	IRAN1583C	–	OQ164838	KC898236	KC898219	N/A
Dothiorella sarmentorum	MFLUCC 13-0498	–	N/A	KJ742379	KJ742382	N/A
Dothiorella sarmentorum	CBS 725.79	–	N/A	KX464130	KX464622	KX464888
Dothiorella sarmentorum	**IMI 63581b**	–	NG_042411	AY573212	AY573235	MT592612
Dothiorella septata	MFLUCC 23-0039	–	OR020695	OR020942	OR030462	OR030480
Dothiorella striata	ICMP 16819	–	N/A	EU673320	EU673287	EU673142
Dothiorella striata	**DAR80992**	–	N/A	KJ573643	KJ573640	N/A
Dothiorella swieteniae	**GBWSCCF120263**		PX499330	PX494348	N/A	N/A
Dothiorella swieteniae	HKAS 151749		PX499331	PX494349	N/A	N/A
Dothiorella tectonae	MFLUCC12-0382	–	N/A	KM396899	KM409637	KM510357
Dothiorella thailandica	**MFLUCC 11-0438**	–	NG_042725	NR_111794	JX646861	JX646844
Dothiorella thripsita	BRIP 51876	–	KX464338	KJ573642	KJ573639	KJ577550
Dothiorella ulmacea	**CBS 138855**	–	KR611899	KR611881	KR611910	KR611909
Dothiorella uruguayensis	**CBS 124908**	–	MH874932	NR_156208	N/A	KX464886
Dothiorella vinea-gemmae	**B116-3**	–	N/A	KJ573644	KJ573641	KJ577552
Dothiorella viticola	**WA10NO01**	–	N/A	HM009376	HM800511	HM800519
Dothiorella viticola	WA10NO02	–	N/A	HM009377	HM800512	HM800520
Dothiorella yunnana	CGMCC 3.18000	–	N/A	KX499644	KX499650	N/A
Dothiorella zanthoxyli	CGMCC 3.24159	–	N/A	OQ190536	OQ241468	OQ275069
Lasiodiplodia crassispora	**CBS 118741**	EU673190	DQ377901	DQ103550	EU673303	N/A
Lasiodiplodia avicenniae	**CMW41467**	N/A	N/A	KP860835	KP860680	N/A
Neofusicoccum luteum	**CBS 562.92**	–	KX464430	KX464170	KX464690	KX464968
Neofusicoccum luteum	**CMW 41365**	–	N/A	NR_147360	KP860702	KP860779

N/A: Sequences not available; "–": Sequences not used for analyses.

861, ITS = 567, *tef*1-α = 157, *β-tubulin* = 430). Both ML and BI analyses exhibit similar tree topologies. The best scoring RAxML tree with a final likelihood value of -8660.703 is presented (Fig. 1). The matrix of combined dataset included

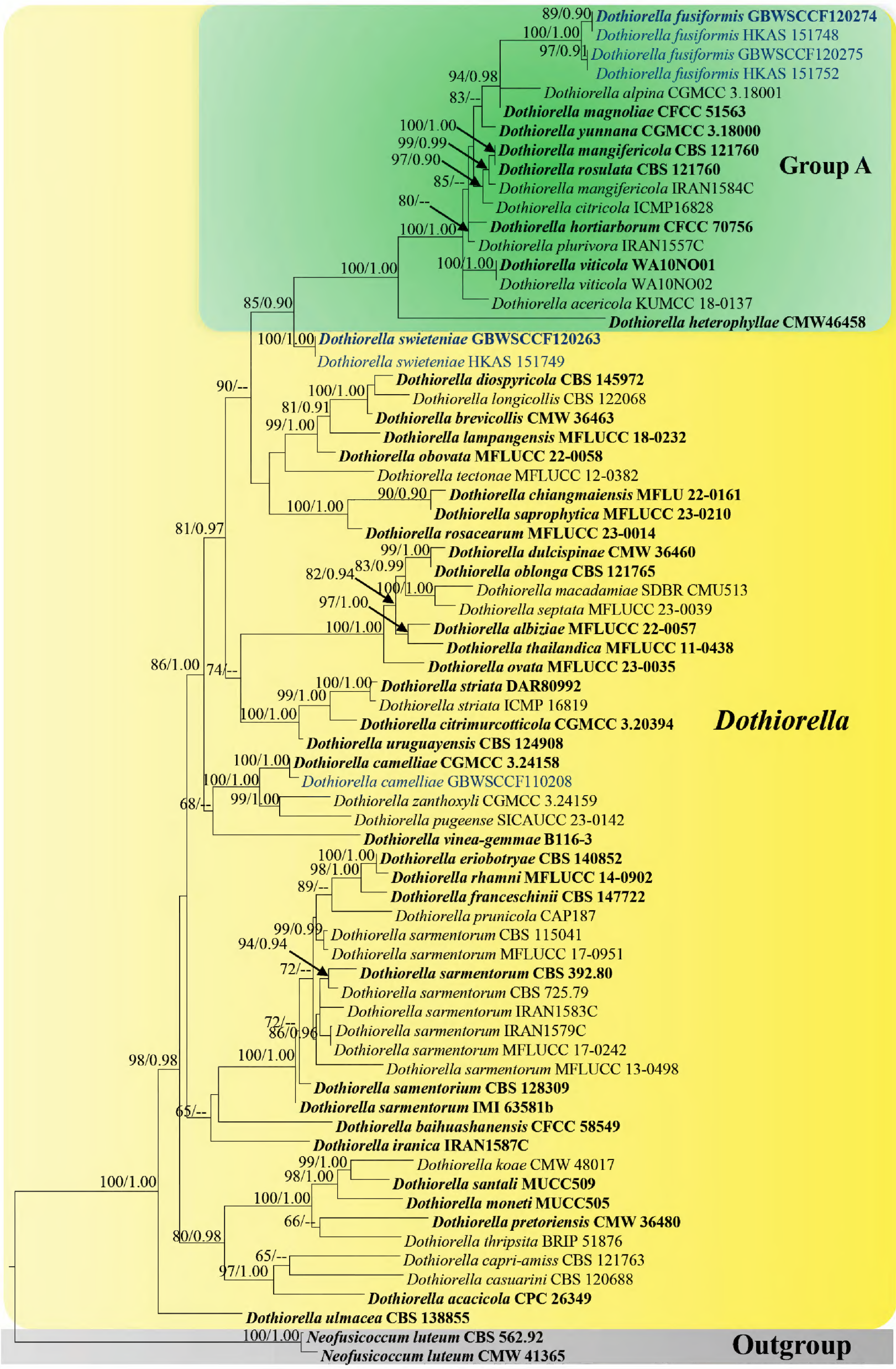

Figure 1. Phylogenetic tree generated from ML analysis based on combined dataset of LSU, ITS, *tef*1-α and *β-tubulin*. The tree is rooted to *Neofusicoccum luteum* (CMW 4165 and CBS 562.26). Bootstrap support values for ML ≥ 65% and Posterior probabilities (PP) ≥ 0.90 are noted at the nodes. Strain numbers are noted after the species names. Strains isolated in this study are represented as blue and type strains are in bold.

579 distinct alignment patterns, with 25.77% undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.218, C = 0.279, G = 0.274, T = 0.229; substitution rates AC = 1.0, AG = 1.97806, AT = 1.0, CG = 1.0, CT = 4.75260, GT = 1.0; gamma distribution shape parameter α = 0.604. In BI analysis, 10,001 trees resulted after 1,000,000 generations. The first 1000 trees, representing the burn-in phase, were discarded, while the remaining 9001 trees were used to calculate posterior probabilities in the majority rule consensus tree. The average standard deviation of split frequencies was 0.01 after 1,000,000 generations of runs. According to the phylogenetic analyses, our new strains (GBWSCCF120274, HKAS 151748, GBWSCCF120275, HKAS 151752, GBWSCCF120263 and HKAS 151749) formed separate clades within *Dothiorella*.

For *Barriopsis*, the combined dataset (SSU, LSU, ITS and *tef*1-α) consisted of 16 taxa was used with *Lasiodiplodia crassispora* (CBS 118741) and *L. avicenniae* (CMW 41467) as the outgroup taxa. Related sequences were obtained from GenBank and Dong et al. (2025). After aligning, the dataset comprised 2,708 characters including gaps (SSU = 1,024, LSU = 849, ITS = 500, *tef*1-α = 335). Topology of the BI tree (not shown) was similar to the ML tree. The best scoring RAxML tree, with a final likelihood value of -5520.171 is shown in Fig. 2.

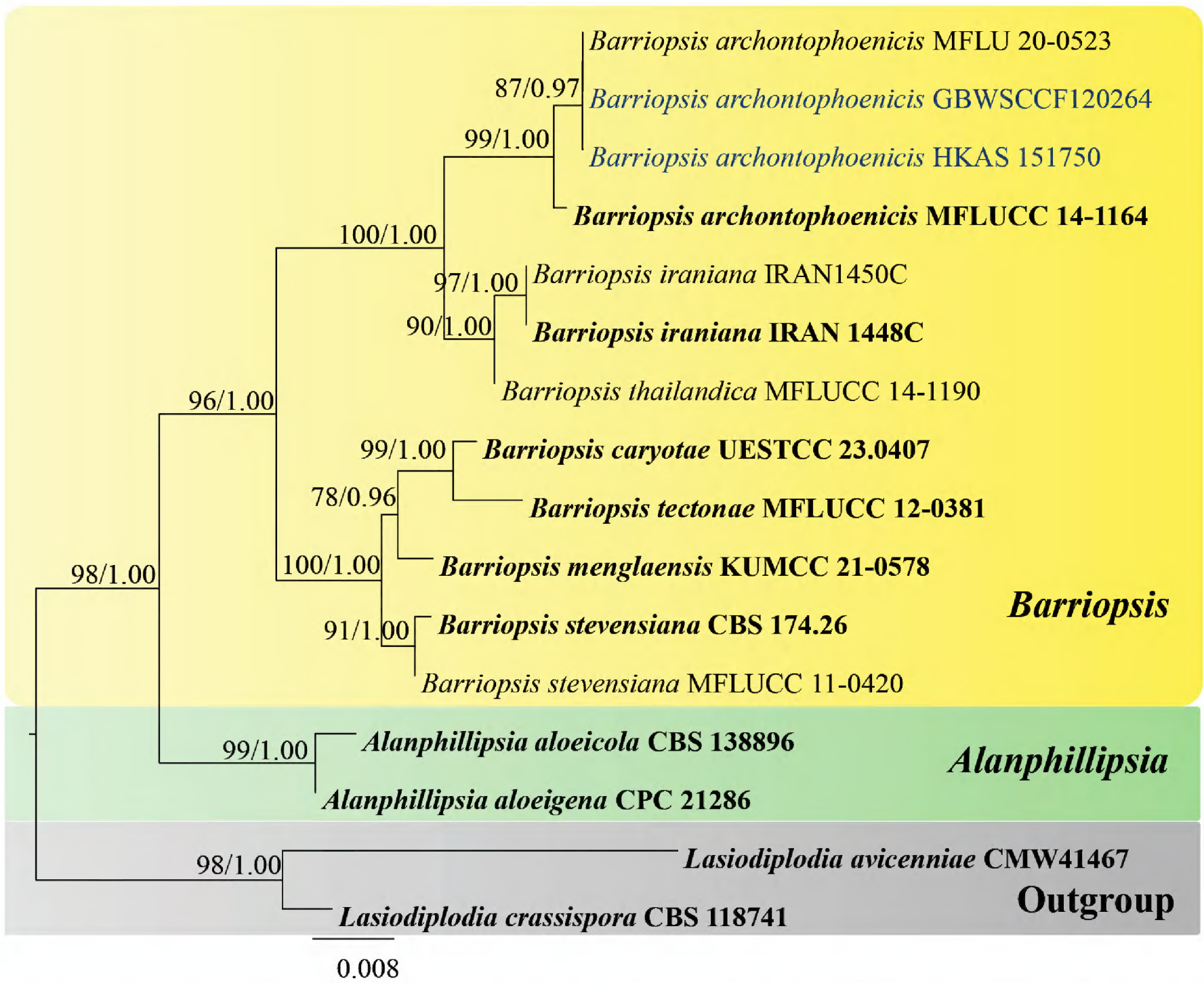

Figure 2. Phylogram generated from ML analysis based on combined dataset of SSU, LSU, ITS and *tef*1-α. The tree is rooted to *Lasiodiplodia crassispora* (CBS 118741) and *L. avicenniae* (CMW 41467). Bootstrap support values for ML ≥ 65% and Bayesian posterior probabilities (PP) ≥ 0.90 are noted at the nodes. Strain numbers are noted after the species names. Strains isolated in this study are represented as blue and type strains are in bold.

The matrix had 295 distinct alignment patterns, with 10.8% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.25, C = 0.25, G = 0.25, T = 0.25; substitution rates AC = 1.0, AG = 2.89532, AT = 1.0, CG = 1.0, CT = 6.81738, GT = 1.0; gamma distribution shape parameter α = 0.176413. In BI analysis, the average standard deviation of split frequencies was 0.001 after 1,000,000 generations of runs.

Taxonomy

Dothiorella fusiformis **Rathnayaka & F. Q. Yu, sp. nov.**
Index Fungorum: IF904781
Figs 3, 4

Etymology. The epithet refers to fusiform-shaped ascospores.

Holotype. HKAS 151748.

Description. ***Saprobic*** on dead twigs of *Thalictrum* sp. ***Sexual morph: Ascomata*** 190–250 µm high × 190–225 µm diam. ($\bar{x}$ = 220 × 200 µm, n = 10), immersed to erumpent through host tissue, globose, solitary and scattered, black, unilocular. ***Peridium*** 20–35 µm wide, composed of two layers, outer layer consists of thick-walled, dark brown to brown cells of *textura angularis*, inner layer composed of thin-walled, pale brown to hyaline cells of *textura angularis*. ***Hamathecium*** comprising numerous 3–5 µm wide, hyaline, septate, unbranched pseudoparaphyses. ***Asci*** 80–91 × 17–20 µm ($\bar{x}$ = 87 × 19 µm, n = 30), 8 or 4-spored, bitunicate, fissitunicate, cylindrical-clavate to clavate, short-pedicellate, apically rounded, with ocular chamber. ***Ascospores*** 13–18 × 6–10 µm ($\bar{x}$ = 16 × 5 µm, n = 30), length/width (l/w) ratio = 3.2, overlapping 2–3-seriate, broadly fusiform, straight or slightly curved, initially hyaline and aseptate, becoming dark brown and 1-septate at maturity, slightly constricted at the septum, rough-walled. ***Asexual morph:*** *Saprobic* on the dead twigs of *Thalictrum* sp. Coelomycetous. ***Conidiomata*** 295–325 µm high × 310–375 µm diam. ($\bar{x}$ = 310 × 350 µm, n = 10), pycnidial, solitary, globose, formed in uniloculate stromata, immersed to erumpent through host tissue. ***Conidiomatal wall*** 20–38 µm diam., 4–6 layers, consists of outer layers of thick-walled, dark brown to brown cells of *textura angularis*, inner layers consists of thin-walled, pale brown to hyaline cells of *textura angularis*. ***Conidiophores*** usually reduced to conidiogenous cells. ***Conidiogenous cells*** 10–4 µm high × 3–5 µm diam. ($\bar{x}$ = 6 × 4 µm, n = 15), lining the pycnidial cavity, holoblastic, hyaline, cylindrical, discrete, determinate, smooth-walled. ***Conidia*** 10–18 × 5–7 µm ($\bar{x}$ = 15 × 6 µm, n = 25, l/w = 2.5), oblong to ellipsoidal, straight or slightly curved, rounded at both ends, initially hyaline and aseptate, becoming dark brown often while attached to conidiogenous cell, slightly constricted at the septum, guttulate.

Culture characteristics. Ascospores germinating on PDA within 24 h. Germ tubes produced at one side of ascospore. Colonies on PDA reaching 3–3.5 cm diam. after 4 days at 25 °C, colonies circular in shape, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, aerial, white in middle and black in outer layer in both upper and lower sides (Fig. 3). Conidia germinating on PDA within 24 h. Germ tubes produced at one side of Conidia. Colonies on PDA reaching 2–3.5 cm diam. after 5 days at 25 °C, colonies circular in shape, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, aerial, black in both upper and lower sides (Fig. 4).

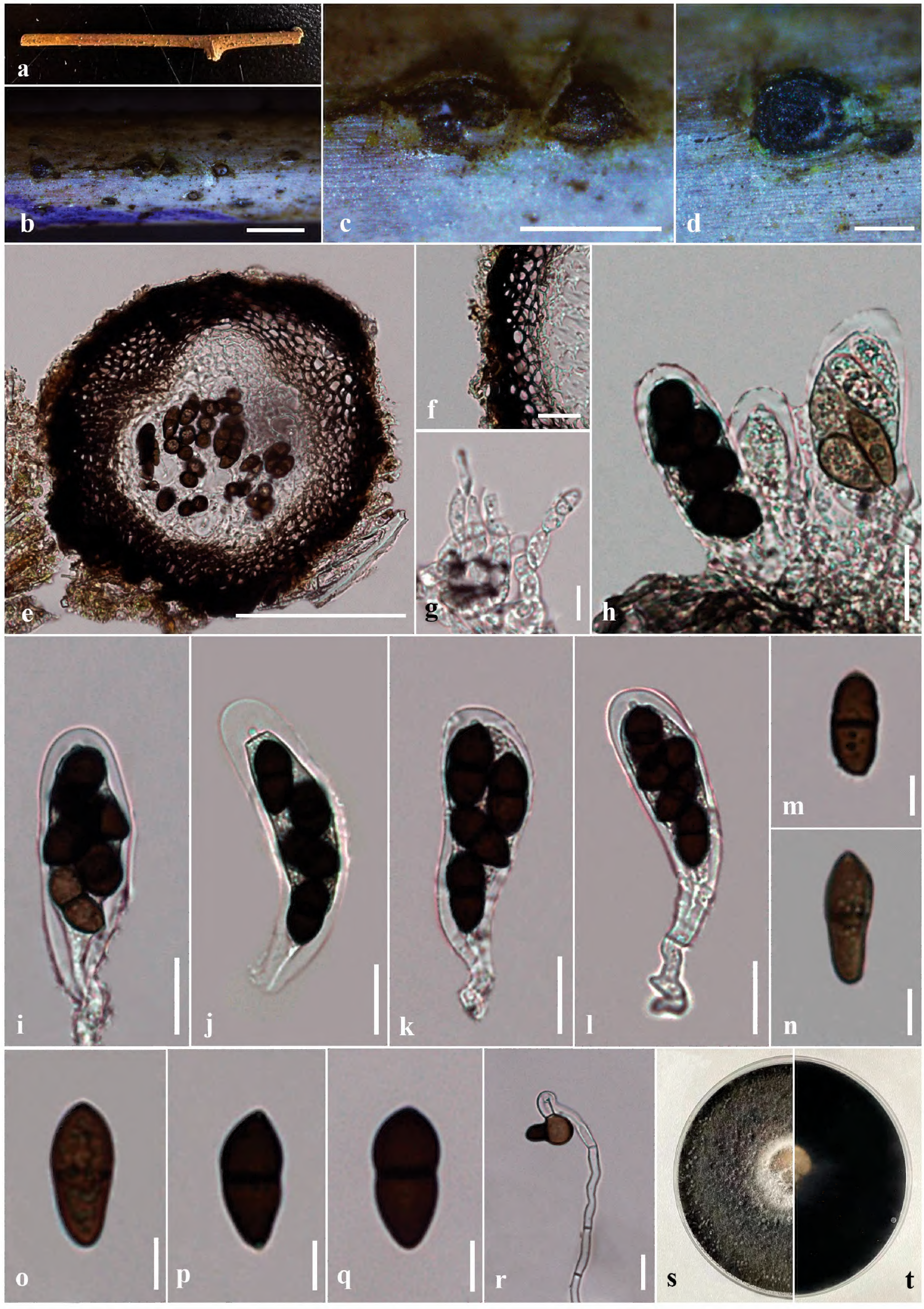

Figure 3. *Dothiorella fusiformis* (HKAS 151748, Holotype, sexual morph) on dead twig of *Thalictrum* sp. **a.** Natural host substrate; **b, c.** Appearance of ascostromata on the host; **d, e.** A section through an ascoma; **f.** Peridium; **g.** Pseudoparaphyses; **h–l.** Asci; **m–q.** Ascospores; **r.** A germinated ascospore; **s, t.** Colony on PDA (**s.** Upper; **t.** Lower views). Scale bars: 1 mm (**b**); 500 µm (**c**); 200 µm (**d**); 100 µm (**e**); 20 µm (**f, h–l**); 10 µm (**g, r**); 5 µm (**m–q**).

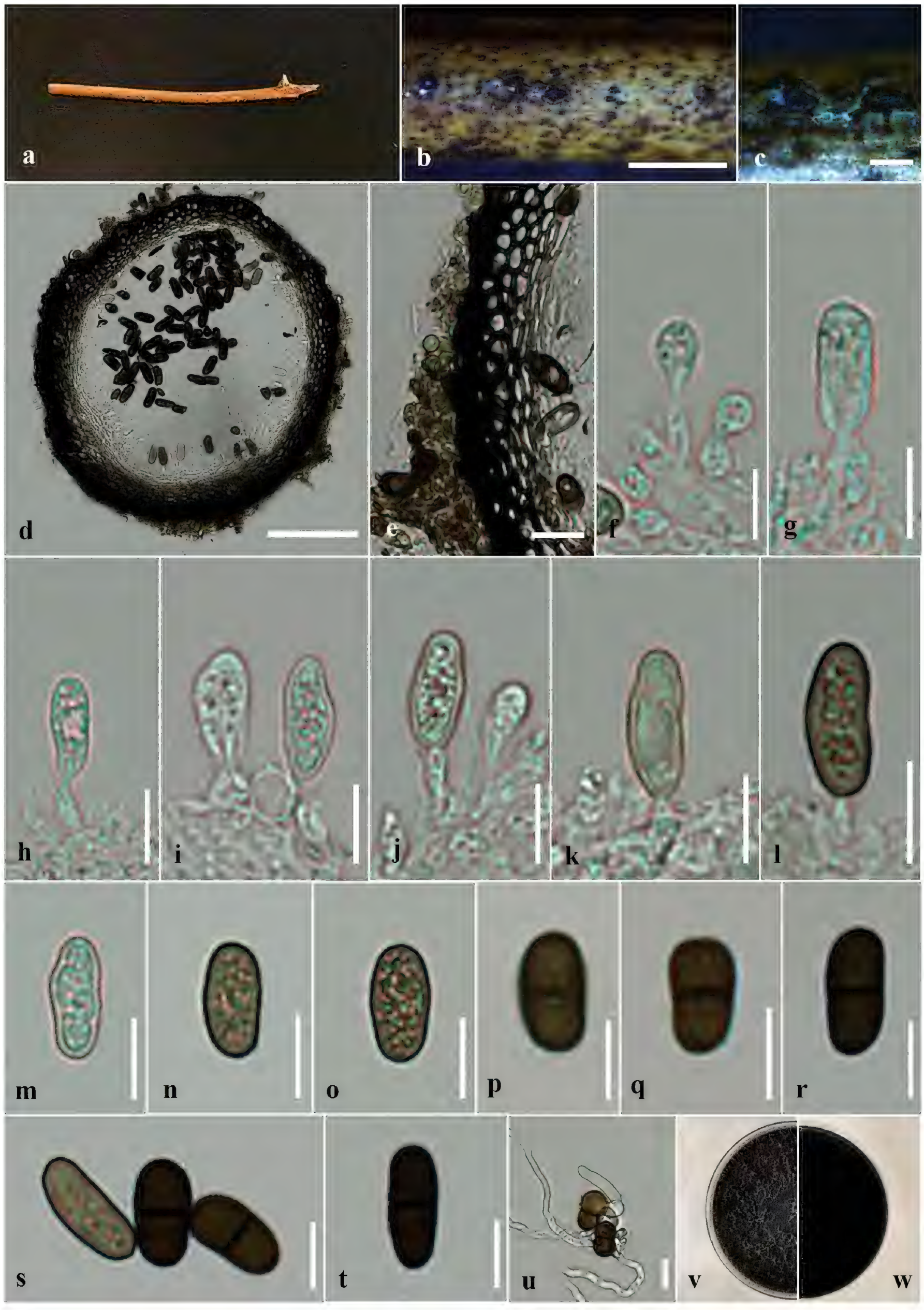

Figure 4. *Dothiorella fusiformis* (HKAS 151752, asexual morph) on dead twig of *Thalictrum* sp. **a.** Natural host substrate; **b, c.** Conidiomata on the host surface; **d.** A vertical section through conidioma; **e.** Peridium of conidioma; **f–l.** Conidia attached to conidiogenous cells; **m–t.** Conidia; **u.** Germinated conidia; **v, w.** Colony on PDA (**v.** Upper; **w.** Lower views). Scale bars: 1 mm (**b**); 200 µm (**c**); 100 µm (**d**); 20 µm (**e**); 10 µm (**f–u**).

Material examined. CHINA • Yunnan Province, Pu'er City, Xiaoheijiang Forest Park, lives on dead twigs of *Thalictrum* sp. (Ranunculaceae), 25 September 2025, Achala Rathnayaka, AS80 (HKAS 151748, **holotype**), ex-type living culture GBWSCCF120274; *ibid*., AS82 (HKAS 151752), living culture GBWSCCF120275.

Notes. In the multi-gene phylogeny of combined LSU, ITS, *tef*1-α and *β-tubulin* analyses, our novel strains (GBWSCCF120274/HKAS 151748/GBWSCCF120275/HKAS 151752) formed a separate clade sister to *D. alpina* (CGMCC 3.18001) with 94% ML bootstrap and 0.98 PP support (Fig. 1, Group A). When comparing the basepair (bp) differences between our new isolate (HKAS 151748) and *D. alpina* (CGMCC 3.18001), ITS shows around 2.1% (10/478) differences (without gaps). Also, bp comparison between HKAS 151748/GBWSCCF120274 and HKAS 151752/GBWSCCF120275 revealed that 0.2% (1/490) and 0.1% (1/852) differences in the ITS and LSU, respectively. Phylogenetically closely related *Dothiorella alpina*, has been recorded only from its asexual morph by Hyde et al. (2020) in *Ipomoea* sp., Yunnan Province, China. Morphologically, the asexual morph of our new collection (HKAS 151752) differs from *D. alpina* (KUN-HKAS 102212) by the size of conidiomata (295–325 µm high × 310–375 µm diam. vs. 135–245 µm high × 150–235 µm diam.) (Hyde et al. 2020). In considering the conidial morphology, *D. fusiformis* has oblong to ellipsoidal, straight or slightly curved conidia that slightly constricted at the septum, guttulate and with l/w ratio of 2.5 (this study). However, in *D. alpina*, the conidia are oblong, occasionally irregular in shape, not constricted at the septa, and with l/w ratio of 2.19 (Hyde et al. 2020). Thus, based on distinct morphology and phylogenetic evidence, we established our new collection, *D. fusiformis* as a new species in *Dothiorella*. Also, in this study, we introduced both sexual (GBWSCCF120274/ HKAS 151748) and asexual (GBWSCCF120275/ HKAS 151752) morphs of *D. fusiformis*.

Dothiorella swieteniae **Rathnayaka & F. Q. Yu, sp. nov.**

Index Fungorum: IF904782

Fig. 5

Etymology. The epithet refers to the host genus "Swietenia", from which the fungus was collected.

Holotype. HKAS 151749.

Description. ***Saprobic*** on dead branches of *Swietenia macrophylla* King. ***Sexual morph*****:** Undetermined. ***Asexual morph*****:** Coelomycetous. ***Conidiomata*** 110–125 µm high × 150–175 µm diam. ($\bar{x}$ = 118 × 163 µm, n = 10) pycnidial, solitary, globose to sub globose, formed in uniloculate stromata, immersed, appear as black dots on host surface, ostiolate. ***Ostiole*** 30–40 µm diam., central, papillate. ***Conidiomatal wall*** 18–37 µm diam., 3–5 layers, consists of outer layers of thick-walled, dark brown to brown cells of *textura angularis*, inner layers consist of thin-walled, pale brown to hyaline cells of *textura angularis*. ***Conidiophores*** usually reduced to conidiogenous cells. ***Conidiogenous cells*** 4–9 µm high × 3–7 µm diam. ($\bar{x}$ = 7 × 5 µm, n = 20), lining the pycnidial cavity, holoblastic, hyaline, cylindrical, discrete, determinate, smooth-walled. ***Conidia*** 14–28 µm high × 7–13 µm diam. ($\bar{x}$ = 21 × 10 µm, n = 20, l/w = 2.1) ellipsoid, straight or slightly curved, rounded at both ends, initially hyaline and aseptate, becoming dark

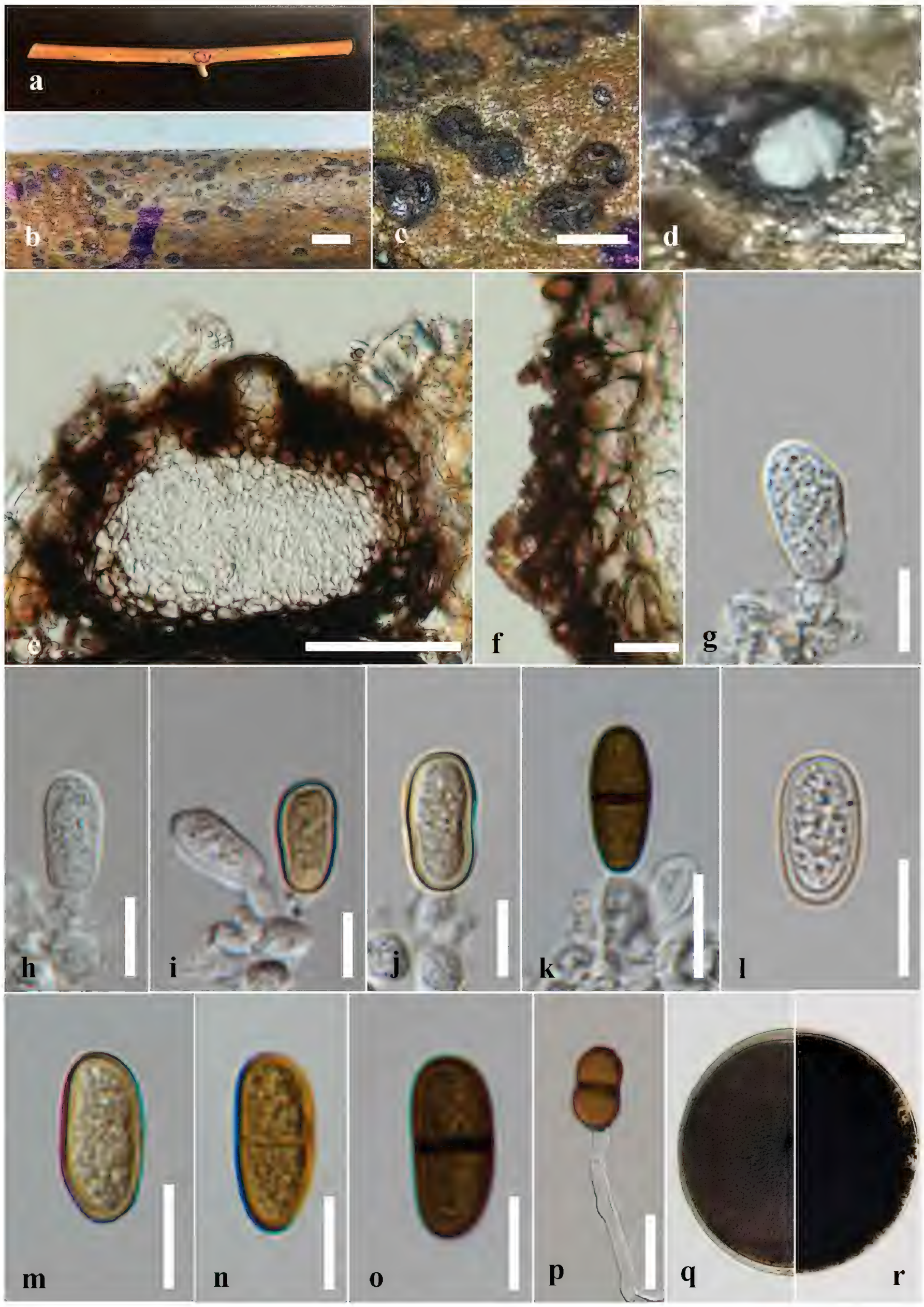

Figure 5. *Dothiorella swieteniae* (HKAS 151749, holotype) on dead branches of *Swietenia macrophylla*. **a.** Natural host substrate; **b, c.** Conidiomata on the host surface; **d, e.** A vertical section through conidioma; **f.** Peridium of conidioma; **g–k.** Conidia attached to conidiogenous cells; **l–o.** Conidia; **p.** A germinated conidium; **q, r.** Colony on PDA (**q.** Upper; **r.** Lower views). Scale bars: 1 mm (**b**); 500 µm (**c**); 100 µm (**d**); 50 µm (**e**); 10 µm (**f–p**).

brown and 1-septate often while attached to conidiogenous cell, slightly constricted at the septum, guttulate.

Culture characteristics. Conidia germinating on PDA within 24 h. Germ tubes produced at one side of Conidia. Colonies on PDA reaching 2–3.5 cm diam. after 6 days at 25 °C, colonies circular in shape, medium dense, flat or effuse, slightly raised, fluffy to fairly fluffy, aerial, black in both upper and lower sides.

Material examined. CHINA • Yunnan Province, Sun River National Forest Park, Pu'er City, lives on dead branches of *Swietenia macrophylla* (Meliaceae), 07 July 2025, Achala Rathnayaka, AS12 (HKAS 151749, **holotype**), ex-type living culture GBWSCCF120263.

Notes. Morphologically, our new collection, *Dothiorella swieteniae* (HKAS 151749 and GBWSCCF120263) fits with the generic concept of *Dothiorella* in having 1-septate, brown conidia attached to the conidiogenous cells (Phillips et al. 2005; Dissanayake et al. 2016). Based on multigene phylogeny (LSU, ITS, *tef*1-α and *β-tubulin*) this novel taxon forms a distinct lineage basal to *Dothiorella* species in group A (Fig. 1), *i.e.*, *Dothiorella acericola* (KUMCC 18-0137), *D. alpina* (CGMCC 3.18001), *D. citricola* (ICMP16828), *D. heterophyllae* (CMW46458), *D. hortiarborum* (CFCC 70756), *D. fusiformis* (GBWSCCF120274), *D. magnoliae* (CFCC 51563), *D. mangifericola* (CBS 121760), *D. plurivora* (IRAN1557C), *D. rosulata* (CBS 121760), *D. viticola* (WA10NO01), and *D. yunnana* (CGMCC 3.18000) with 85% ML and 0.90 PP statistical support values (Fig. 1). Detailed morphological comparison between species in group A and *D. swieteniae* is provided in Table 3. The l/w ratio (2.1) of conidia in *D. swieteniae* (HKAS 151749) is similar to *D. alpina*, *D. citricola* and *D. mangifericola* (Table 3). However, when considering the shape and verruculose surface of the conidia, *D. swieteniae* differs from *D. alpina*, *D. citricola* and *D. mangifericola* (Table 3). Thus, considering the morpho-molecular data analysis, we established *D. swieteniae* as a new species in *Dothiorella*.

Dothiorella camelliae **W.Li Li & Jian K. Liu (2023)**

Index Fungorum: IF847167

Fig. 6

Description. ***Saprobic*** on dead branches of *Macaranga peltata*. ***Sexual morph*****:** ***Ascomata*** 125–150 × 100–225 µm ($\bar{x}$ = 150 × 140 µm, n = 10), immersed to erumpent through host tissue, globose, solitary and scattered, black, multilocular or unilocular. ***Peridium*** 15–46 µm wide, composed of two layers, outer layer consists of thick-walled, brown to dark-brown cells of *textura angularis*, inner layer consists of thin-walled, pale brown to hyaline cells of *textura angularis*. ***Hamathecium*** comprising numerous 3–4 µm wide, hyaline, frequently aseptate pseudoparaphyses. ***Asci*** 72–90 × 20–25 µm ($\bar{x}$ = 80 × 23 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical-clavate to clavate, short-pedicellate, apically rounded, with ocular chamber. ***Ascospores*** 18–25 × 9–12 µm ($\bar{x}$ = 22 × 11 µm, n = 30, l/w ratio = 2), overlapping 2–3-seriate, oblong, ovate to sub-clavate, straight or slightly curved, initially hyaline and aseptate and becoming dark brown and 1-septate at maturity, slightly constricted at the septum, rough-walled. ***Asexual morph*****:** Undetermined.

Table 3. Synopsis of morphological characters of conidia among the *Dothiorella swieteniae* and species in group A.

Species	Conidia				Reference(s)
	Size (µm)	Average (µm)	Ratio (L/W)	Characters	
Dothiorella acericola	17–22(–23) × 7–10(–13)	20.8 × 9.2	2.2	Oblong to ellipsoidal, 1-septate, slightly constricted at the septum, smooth-walled	Phookamsak et al. (2019)
D. alpina	22–25(–28) × 10–12(–13)	24.4 × 11.1	2.1	Oblong with rounded ends, occasionally irregular in shape, 1-septate, smooth-walled	Hyde et al. (2020)
D. citricola	24–27 × 10–12	25.8 × 12.2	2.1	Oblong to subcylindrical, 1-septate, occasionally slightly constricted at septum, moderately thick walled, externally smooth, internally finely verruculose, ends truncate	Abdollahzadeh et al. (2014)
D. heterophyllae	18–26 × 8.5–11.5	22.6 × 9.8	2.3	Ellipsoidal, tapering towards a truncated base, 1-septate, septum median, verruculous	Jami et al. (2019)
D. hortiarborum	10.0–19.0 × 6.0–11.0	14.9 ± 2.6 × 8.1 ± 1.0	1.8	Ovoid with a broadly rounded apex, truncate base, uneven surface, thick-walled, 1-septate, constricted at the septum	Wu et al. (2024)
D. fusiformis	10–18 × 5–7	15 × 6	2.5	Oblong to ellipsoidal, straight or slightly curved, 1-septate slightly constricted at the septum, guttulate	This study
D. magnoliae	20.6–22.5 × 10.9–12.0	21.56 × 11.45	1.9	Internally finely verruculose, 1-septate, always deeply constricted at septum, externally smooth	You et al. (2017)
D. mangifericola	17–22 × 8–10	19 × 9	2.1	Subcylindrical to ellipsoid or ovoid, 1-septate, occasionally slightly constricted at septum, internally finely verruculose	Abdollahzadeh et al. (2014)
D. plurivora	(17–)18.7–20.6(–21) × (8–)8.5–9.7(–11)	19.7 × 9	2.2	Ellipsoid to ovoid, straight, 1-septate, slightly constricted at the septum, rounded at both ends	Hyde et al. (2024)
D. rosulata	(19–)21–24.2(–26.7) × (8–)10–10.5(–13)	22.6 × 10.4	2.2	Ovoid to subcylindrical or ellipsoidal, 1-septate, occasionally constricted at the septum, moderately thick-walled, smooth, mostly guttulate	Slippers et al. (2014)
D. swieteniae	14–28 × 7–13	21 × 10	2.1	Ellipsoid, straight or slightly curved, 1-septate, slightly constricted at the septum, guttulate	This study
D. viticola	(17.5–)19.5–23(–28.5) × (9–)10.5–12.5(–14)	21.3 × 11.4	1.9	Subcylindrical to ellipsoid or ovoid, 1-septate, occasionally slightly constricted at septum, moderately thick-walled, externally smooth, internally finely verruculose, ends rounded, often with a truncate base	Zhang et al. (2021)
D. yunnana	19.6–21 × 8.6–9.2	20.3 × 8.9	2.3	Ellipsoid, 1-septate, externally smooth, occasionally slightly constricted at the septum with rounded apex and truncate base	Zhang et al. (2016)

Culture characteristics. Ascospores germinating on PDA within 24 h. Germ tubes produced at one side of ascospore. Colonies on PDA reaching 2–3.5 cm diam. after 6 days at 25 °C, colonies circular in shape, medium dense,

Figure 6. *Dothiorella camelliae* (HKAS 151751, a new host record) on dead branch of *Macaranga peltata*. **a.** Natural host substrate; **b, c.** Appearance of ascostromata on host; **d.** A section through ascostromata; **e.** A cross section of an ascoma; **f.** Peridium; **g.** Pseudoparaphyses; **h–m.** Asci; **n–q.** Ascospores; **r.** A germinated ascospore; **s, t.** Colony on PDA (**s.** Upper; **t.** Lower views). Scale bars: 2 mm (**b**); 500 µm (**c**); 200 µm (**d**); 50 µm (**e**); 20 µm (**h–m, r**); 10 µm (**f, g, n–q**).

flat or effuse, slightly raised, fluffy to fairly fluffy, aerial, black in both upper and lower sides.

Material examined. CHINA • Yunnan Province, Pu'er City, lives on dead branches of *Macaranga peltata* Roxb. Mueller (Euphorbiaceae), 06 July 2025, Achala Rathnayaka, AS27 (HKAS 151751), living culture GBWSCCF110208.

Notes. Based on multigene phylogenetic analyses (LSU, ITS, *tef*1-α and *β-tubulin*), our new strain (GBWSCCF110208) clustered with the ex-type strain of *D. camelliae* (CGMCC 3. 24158) with 100% ML and 1.00 PP statistical support (Fig. 1). Morphologically, our collection is similar to the holotype of *D. camelliae* (HKAS 125892), which was collected from decaying branches of *Camellia oleifera* in Sichuan Province, China (Li et al. 2023). Both strains have solitary or gregarious, globose, black, multilocular or unilocular ascomata; hyaline, aseptate pseudoparaphyses; clavate asci; and oblong, ovate to sub-clavate, dark brown ascospores (Li et al. 2023). Previously, *D. camelliae* was recorded on dead branches of *Camellia oleifera* and *Paeonia suffruticosa* in Sichuan and Shandong Provinces, China, respectively (Li et al. 2023). We determined our collection as a new host record of *D. camelliae* from *Macaranga peltata* in Yunnan Province, China.

***Barriopsis archontophoenicis* S. Konta, Boonmee & K.D. Hyde (2016)**

Index Fungorum: IF552104

Fig. 7

Description. ***Saprobic*** on dead twig of *Clarisia racemosa*. ***Sexual morph*: *Ascomata*** 220–280 µm, high × 220–245 µm diam ($\bar{x}$ = 260 × 225 µm, n = 10), solitary to aggregated, immersed, erumpent at maturity, uniloculate, subglobose, black, papillate. ***Peridium*** 25–60 µm wide, 3–5 layers, composed of outer layers of thick-walled, dark brown cells of *textura angularis*, inner layers composed of thin-walled, hyaline cells of *textura angularis*. ***Hamathecium*** comprising numerous 3–5 µm wide, hypha-like, septate, cellular pseudoparaphyses. ***Asci*** 75–140 × 20–34 µm ($\bar{x}$ = 115 × 26 µm, n = 15), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apically rounded, with well development ocular chamber. ***Ascospores*** 23–30 × 8–11 µm ($\bar{x}$ = 24 × 9.8 µm, n = 30, l/w = 2.4), overlapping 2–3-seriate, ellipsoid to ovoid, broad at the middle, aseptate, rough-walled, initially hyaline, with a large central guttule, becoming dark brown at maturity. ***Asexual morph*:** Undetermined.

Culture characters. Ascospores germinating on PDA within 6 hours and germ tube produced from one end of the ascospore. Colonies on PDA reaching 6–8 cm diam. after 10 days at 25 °C, colonies irregular in shape, flat or effuse, slightly raised, pale yellow at the edge, black in both upper and lower sides.

Material examined. CHINA • Yunnan Province, Sun River National Forest Park, Pu'er City, on a dead twig of *Clarisia racemosa* (Moraceae), 07 July 2025, Achala Rathnayaka, AS14 (HKAS 151750), living culture GBWSCCF120264.

Notes. The specimen examined in this study has similar morphology to the holotype of *Barriopsis archontophoenicis*, collected from *Archontophoenix alexandrae* in Thailand (Konta et al. 2016). Both isolates have solitary to aggregated, immersed ascomata, cylindrical-clavate, short-pedicellate, apically rounded

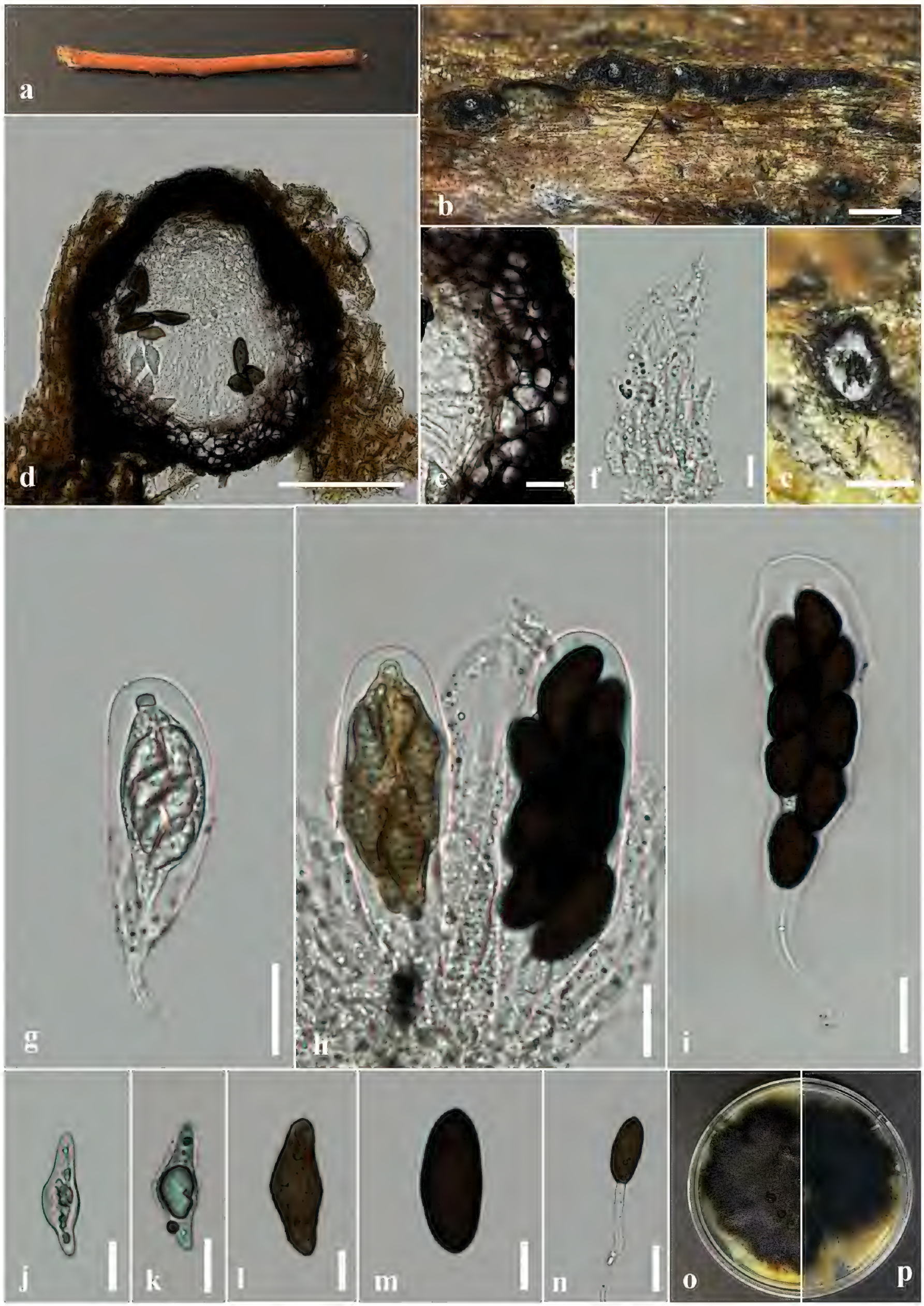

Figure 7. *Barriopsis archontophoenicis* (HKAS 151750, a new host record) on dead branch of *clarisia racemosa*. **a.** Natural host substrate; **b.** Appearance of ascostroma on the host substrate; **c, d.** A section through an ascoma; **e.** Peridium; **f.** Pseudoparaphyses; **g–i.** Asci; **j–m.** Ascospores; **n.** A germinated ascospore; **o, p.** Colony on PDA (**o.** Upper; **p.** Lower views). Scale bars: 200 µm (**b, c**); 100 µm (**d**); 20 µm (**g–i, n**); 10 µm (**e**, **f, j–m**).

asci, with a well-developed ocular chamber. Ascospores are ellipsoid to ovoid, broader at the middle, aseptate, and dark brown (Konta et al. 2016). Ascospore sizes are similar in both holotype and our collection ($\overline{x}$ = 22 × 9 vs. $\overline{x}$ = 24 × 9.8 µm, l/w = 2.4) (Konta et al. 2016). Based on the phylogenetic analyses, our strains of *B. archontophoenicis* (GBWSCCF120264 and HKAS 151750) clustered with the ex-type and other strain of *B. archontophoenicis* (MFLUCC 14-1164 and MFLU 20-0523) with 87% ML and 0.97 PP statistical support (Fig. 2). Previously, *B. archontophoenicis* have been recorded in *A. alexandrae* in Thailand (Konta et al. 2016) and *Camellia sinensis* in Taiwan province, China (Rathnayaka et al. 2021). Based on morpho-molecular analyses, we reported our collection as a new host record of *B. archontophoenicis* on *Clarisia racemosa* in China.

Discussion

Saprobic fungi are ecologically important due to their critical role in decomposition and nutrient cycling. Ascomycota is considered one of the most representative fungal groups involved in saprobic behavior (Benny et al. 2001; Li et al. 2022). Investigating saprobic fungi is essential, as it helps in understanding their ecological roles and also discovering their hidden diversity (Du et al. 2025). Tropical forests have rich Ascomycota diversity, and Yunnan Province is dominated by tropical lower montane broad-leaved evergreen forests (Tedersoo et al. 2014; Zhu et al. 2021; Li et al. 2022). Therefore, Yunnan Province contains a rich diversity of Ascomycota. Feng and Yang (2018) mentioned that only around 6,000 of the estimated 104,000 fungal species have been described in Yunnan Province, and about 95% of the hidden fungal diversity still remain to be explored. Thus, studying saprobic Ascomycota in Yunnan Province is important.

Saprobic fungal species were collected from terrestrial habitats in Yunnan Province, China, from July – September 2025 from different forest areas, under tropical climatic conditions. Based on morphological characterization and molecular phylogeny, we introduced two new species and one new host record in *Dothiorella*; namely, *D. fusiformis*, *D. swieteniae* and *D. camelliae*, respectively. We provide complete morphological descriptions for both sexual and asexual morphs for *D. fusiformis*. Additionally, *Barriopsis archontophoenicis* is described as a new host record from *Clarisia racemosa* in Yunnan Province, China.

The genus *Dothiorella* accommodates fungal species characterized by conidia that develop pigmentation while attached to their conidiogenous cells (Phillips et al. 2005). Concurrently, *Spencermartinsia* was introduced to include *Dothiorella*-like taxa that have apiculate ascospores (Phillips et al. 2008). However, apiculate ascospores were considered unreliable for generic delineation (Yang et al. 2017). Therefore, with the support of multi-gene phylogenetic analyses, *Spencermartinsia* was synonymized with *Dothiorella* (Dissanayake et al. 2016; Zhang et al. 2016; Yang et al. 2017). Later, Zhou et al. (2025) showed that *Spencermartinsia* is a synonym of *Dothiorella* based on their comprehensive phylogenetic analyses.

In the recent decade, several species of *Dothiorella* have been described in China, including *D. acericola* on dead hanging twigs of *Acer palmatum* (Phookamsak et al. 2019), *D. baihuashanensis* on dead branches of *Juniperus chinensis* (Lin et al. 2023), *D. camelliae* on decaying branches of *Camellia oleifera* (Li et al. 2023), *D. hortiarborum* on dead branches of *Fraxinus chinensis* (Wu

et al. 2024), *D. magnoliae* on twigs and branches of *Magnolia grandiflora* (You et al. 2017), *D. pugeense* on dead branches of *Juglans regia* saprobes (Wang et al. 2025), and *D. zanthoxyli* on decaying branches of *Zanthoxylum bungeanum* (Li et al. 2023). Most of these taxa were isolated from dead or decaying woody materials and are recorded as saprobes, except *D. magnoliae* (recorded as pathogens).

Several *Dothiorella* species have been reported as plant pathogens in China. *Dothiorella alpina*, *D. citrimurcotticola*, and *D. plurivora* were isolated from citrus branch diseases (Xiao et al. 2021). *Dothiorella acericola* has been associated with branch cankers of *Ziziphus jujuba* in Beijing, China (Pan et al. 2021), and *D. sarmentorum* was reported to cause leaf spot on *Lavandula angustifolia* in China (Li et al. 2024). In addition, *D. vidmadera*, *D. yunnana*, and *D. zanthoxyli* were isolated from cankered branches of *Chaenomeles cathayensis*, *Rosa chinensis*, and *Diospyros lotus*, respectively (Zhou et al. 2025). However, documentation of *Dothiorella* species as endophytes in China is lacking. Within *Barriopsis*, only *B. menglaense* has been introduced from China, occurring on woody twigs of *Castanopsis mekongensis* (Dong et al. 2025).

Introducing both the sexual and asexual morph of a new fungal species ensures comprehensive identification and accurate taxonomic classification. This study led to the expansion of the taxonomic framework and ecological relationships of Botryosphaeriaceae taxa in China by revealing a new species and two new host records. Therefore, these findings contribute to advancing our understanding of fungal species diversity in China. However, further investigations are needed to discover the hidden diversity of Botryosphaeriaceae species in China.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Conceptualization: ARR, Data curation: ARR, Formal analysis: ARR, ZYY, Funding acquisition: ICS, FQY, Investigation: ARR, SPW, Methodology: ARR, Project administration: SMY, JY, Resources: ICS, FQY, XFS, Software: ARR, Validation: ARR, Visualization: ARR, Writing – original draft: ARR, Writing – review and editing: ARR, ICS, FQY, JWL, DQD.

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Data availability

All of the data that support the findings of this study are available in the main text.

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